



sequence.listing.ST25.txt
SEQUENCE LISTING

<110> McCray, Paul B.
Sanders, David A.
Jeffers, Scott A.
Davidson, Beverly L.
Sinn, Patrick L.

<120> PSEUDOTYPED VIRUSES AND METHODS FOR THEIR USE

<130> 290.00670120

<140> US 10/811,353

<141> 2004-03-26

<160> 16

<170> PatentIn version 3.2

<210> 1

<211> 681

<212> PRT

<213> Marburg virus glycoprotein

<400> 1

Met Lys Thr Thr Cys Phe Leu Ile Ser Leu Ile Leu Ile Gln Gly Thr
1 5 10 15

Lys Asn Leu Pro Ile Leu Glu Ile Ala Ser Asn Asn Gln Pro Gln Asn
20 25 30

Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
35 40 45

Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
50 55 60

Glu Ala Ser Lys Arg Trp Ala Phe Arg Thr Gly Val Pro Pro Lys Asn
65 70 75 80

Val Glu Tyr Thr Glu Gly Glu Glu Ala Lys Thr Cys Tyr Asn Ile Ser
85 90 95

Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro Thr Asn
100 105 110

Ile Arg Asp Tyr Pro Lys Cys Lys Thr Ile His His Ile Gln Gly Gln
115 120 125

Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
130 135 140

Leu Tyr Asp Arg Ile Ala Ser Thr Thr Met Tyr Arg Gly Lys Val Phe
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```

145                               150                               155                               160
Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Lys
                165                170                175
Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
                180                185                190
Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Gly Thr Gln Thr Asn Asp
                195                200                205
Thr Gly Cys Phe Gly Ala Leu Gln Glu Tyr Asn Ser Thr Lys Asn Gln
                210                215                220
Thr Cys Ala Pro Ser Lys Ile Pro Pro Pro Leu Pro Thr Ala Arg Pro
                225                230                235
Glu Ile Lys Leu Thr Ser Thr Pro Thr Asp Ala Thr Lys Leu Asn Thr
                245                250                255
Thr Asp Pro Ser Ser Asp Asp Glu Asp Leu Ala Thr Ser Gly Ser Gly
                260                265                270
Ser Gly Glu Arg Glu Pro His Thr Thr Ser Asp Ala Val Thr Lys Gln
                275                280                285
Gly Leu Ser Ser Thr Met Pro Pro Thr Pro Ser Pro Gln Pro Ser Thr
                290                295                300
Pro Gln Gln Gly Gly Asn Asn Thr Asn His Ser Gln Asp Ala Val Thr
                305                310                315
Glu Leu Asp Lys Asn Asn Thr Thr Ala Gln Pro Ser Met Pro Pro His
                325                330                335
Asn Thr Thr Thr Ile Ser Thr Asn Asn Thr Ser Lys His Asn Phe Ser
                340                345                350
Thr Leu Ser Ala Pro Leu Gln Asn Thr Thr Asn Asp Asn Thr Gln Ser
                355                360                365
Thr Ile Thr Glu Asn Glu Gln Thr Ser Ala Pro Ser Ile Thr Thr Leu
                370                375                380
Pro Pro Thr Gly Asn Pro Thr Thr Ala Lys Ser Thr Ser Ser Lys Lys
                385                390                395                400

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Gly Pro Ala Thr Thr Ala Pro Asn Thr Thr Asn Glu His Phe Thr Ser
405 410 415

Pro Pro Pro Thr Pro Ser Ser Thr Ala Gln His Leu Val Tyr Phe Arg
420 425 430

Arg Lys Arg Ser Ile Leu Trp Arg Glu Gly Asp Met Phe Pro Phe Leu
435 440 445

Asp Gly Leu Ile Asn Ala Pro Ile Asp Phe Asp Pro Val Pro Asn Thr
450 455 460

Lys Thr Ile Phe Asp Glu Ser Ser Ser Ser Gly Ala Ser Ala Glu Glu
465 470 475 480

Asp Gln His Ala Ser Pro Asn Ile Ser Leu Thr Leu Ser Tyr Phe Pro
485 490 495

Asn Ile Asn Glu Asn Thr Ala Tyr Ser Gly Glu Asn Glu Asn Asp Cys
500 505 510

Asp Ala Glu Leu Arg Ile Trp Ser Val Gln Glu Asp Asp Leu Ala Ala
515 520 525

Gly Leu Ser Trp Ile Pro Phe Phe Gly Pro Gly Ile Glu Gly Leu Tyr
530 535 540

Thr Ala Val Leu Ile Lys Asn Gln Asn Asn Leu Val Cys Arg Leu Arg
545 550 555 560

Arg Leu Ala Asn Gln Thr Ala Lys Ser Leu Glu Leu Leu Leu Arg Val
565 570 575

Thr Thr Glu Glu Arg Thr Phe Ser Leu Ile Asn Arg His Ala Ile Asp
580 585 590

Phe Leu Leu Thr Arg Trp Gly Gly Thr Cys Lys Val Leu Gly Pro Asp
595 600 605

Cys Cys Ile Gly Ile Glu Asp Leu Ser Lys Asn Ile Ser Glu Gln Ile
610 615 620

Asp Gln Ile Lys Lys Asp Glu Gln Lys Glu Gly Thr Gly Trp Gly Leu
625 630 635 640

Gly Gly Lys Trp Trp Thr Ser Asp Trp Gly Val Leu Thr Asn Leu Gly
645 650 655

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Ile Leu Leu Leu Leu Ser Ile Ala Val Leu Ile Ala Leu Ser Cys Ile
660 665 670

Cys Arg Ile Phe Thr Lys Tyr Ile Gly
675 680

<210> 2

<211> 2046

<212> DNA

<213> Marburg virus glycoprotein

<400> 2

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ctccagaaga cagaagatgt ccatctgatg ggattcacac tgagtgggca aaaagttgct	180
gattcccctt tggaggcatc caagcgatgg gctttcagga caggtgtacc tccaagaat	240
gttgagtata cagaagggga ggaagccaaa acatgctaca atataagtgt aacggatccc	300
tctggaaaat ccttgctgtt ggatcctcct accaacaatcc gtgactatcc taaatgcaaa	360
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ggagcatttt tcctgtatga tcgcattgcc tccacaacaa tgtaccgagg cagagtcttc	480
actgaaggga acatagcagc tatgattgtc aataagacag tgcacaaaat gattttctcg	540
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aacaatggaa cacaaacgaa tgacactgga tgcttcggtg ctcttcaaga atacaactcc	660
acgaagaatc aaacatgtgc tccgtccaaa ataccctcac cactgcccac agcccgtcca	720
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acttcagatg cggtcactaa gcaagggctt tcatcaacaa tgccaccac tccctcacca	900
caaccaagca cgccacagca agaaggaaac aacacagacc attcccaagg tactgtgact	960
gaaccaaca aaaccaacac aacggcacia ccgtccatgc cccccacaa caccactgca	1020
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accaccaatt acgacacaca gagcacagcc actgaaaatg aacaaaccag tgccccctcg	1140
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cccaaccga ccacacaaca tcttgatat ttcagaaaga aacgaagtat cctctggagg	1320
gaaggcgaca tgtttccttt tctggacggg ttaataaatg ctccaattga ttttgatcca	1380
gttccaaata caaagacgat ctttgatgaa tcttctagtt ctggtgcttc ggctgaggaa	1440

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gatcaacatg cctcccccaa tatcagttta actttatcct attttcctaa tataaatgaa 1500
aacactgcct actctggaga aaatgagaac gattgtgatg cagagttaag aatttgagc 1560
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gaaggacttt atactgctgg ttttaattaaa aacaaaaaca atttggtctg caggttgagg 1680
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aggacatttt ccttaattaa tagacatgcc attgactttc tactcacaag gtggggagga 1800
acatgcaaag tgcttgacc tgattgttgc attggaatag aagacttgtc caggaatatt 1860
tcggaacaaa ttgaccaaat caaaaaagat gaacaaaaag aggggactgg ttggggctta 1920
ggtggtaaat ggtggacatc cgactggggt gttcttacta acttgggcat tttgctacta 1980
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gggtaa 2046

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```

<210> 3
<211> 676
<212> PRT
<213> Ebola virus glycoprotein
<400> 3

```

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Met Gly Val Thr Gly Ile Leu Gln Leu Pro Arg Asp Arg Phe Lys Arg
1          5          10          15

```

```

Thr Ser Phe Phe Leu Trp Val Ile Ile Leu Phe Gln Arg Thr Phe Ser
20          25          30

```

```

Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Asp Val
35          40          45

```

```

Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu Arg
50          55          60

```

```

Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val Pro
65          70          75          80

```

```

Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys Val
85          90          95

```

```

Val Asn Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu Glu
100          105          110

```

```

Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Ala Ala Pro Asp Gly
115          120          125

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Ile Arg Gly Phe Pro Arg Cys Arg Tyr Val His Lys Val Ser Gly Thr
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130

135

140

Gly Pro Cys Ala Gly Asp Phe Ala Phe His Lys Glu Gly Ala Phe Phe
145 150 155 160

Leu Tyr Asp Arg Leu Ala Ser Thr Val Ile Tyr Arg Gly Thr Thr Phe
165 170 175

Ala Glu Gly Val Val Ala Phe Leu Ile Leu Pro Gln Ala Lys Lys Asp
180 185 190

Phe Phe Ser Ser His Pro Leu Arg Glu Pro Val Asn Ala Thr Glu Asp
195 200 205

Pro Ser Ser Gly Tyr Tyr Ser Thr Thr Ile Arg Tyr Gln Ala Thr Gly
210 215 220

Phe Gly Thr Asn Glu Thr Glu Tyr Leu Phe Glu Val Asp Asn Leu Thr
225 230 235 240

Tyr Val Gln Leu Glu Ser Arg Phe Thr Pro Gln Phe Leu Leu Gln Leu
245 250 255

Asn Glu Thr Arg Tyr Thr Ser Gly Lys Arg Ser Asn Thr Thr Gly Lys
260 265 270

Leu Ile Trp Lys Val Asn Pro Glu Ile Asp Thr Thr Ile Gly Glu Trp
275 280 285

Ala Phe Trp Glu Thr Lys Lys Asn Leu Thr Arg Lys Ile Arg Ser Glu
290 295 300

Glu Leu Ser Phe Thr Ala Val Ser Asn Arg Ala Lys Asn Ile Ser Gly
305 310 315 320

Gln Ser Pro Ala Arg Thr Ser Ser Asp Pro Gly Thr Asn Thr Thr Thr
325 330 335

Glu Asp His Lys Ile Met Ala Ser Glu Asn Ser Ser Ala Met Val Gln
340 345 350

Val His Ser Gln Gly Arg Glu Ala Ala Val Ser His Leu Thr Thr Leu
355 360 365

Ala Thr Ile Ser Thr Ser Leu Arg Pro Pro Ile Thr Lys Pro Gly Pro
370 375 380

sequence.listing.ST25.txt

```

Asp Asn Ser Thr His Asn Thr Pro Val Tyr Lys Leu Asp Ile Ser Glu
385          390          395          400

Ala Thr Gln Val Glu Gln His His Arg Arg Thr Asp Asn Ala Ser Thr
          405          410          415

Thr Ser Asp Thr Pro Pro Ala Thr Thr Ala Ala Gly Pro Leu Lys Ala
          420          425          430

Glu Asn Thr Asn Thr Ser Lys Gly Thr Asp Leu Leu Asp Pro Ala Thr
          435          440          445

Thr Thr Ser Pro Gln Asn His Ser Glu Thr Ala Gly Asn Asn Asn Thr
          450          455          460

His His Gln Asp Thr Gly Glu Glu Ser Ala Ser Ser Gly Lys Leu Gly
465          470          475          480

Leu Ile Thr Asn Thr Ile Ala Gly Val Ala Gly Leu Ile Thr Gly Gly
          485          490          495

Arg Arg Thr Arg Arg Glu Ala Ile Val Asn Ala Gln Pro Lys Cys Asn
          500          505          510

Pro Asn Leu His Tyr Trp Thr Thr Gln Asp Glu Gly Ala Ala Ile Gly
          515          520          525

Leu Ala Trp Ile Pro Tyr Phe Gly Pro Ala Ala Glu Gly Ile Tyr Ile
          530          535          540

Glu Gly Leu Met His Asn Gln Asp Gly Leu Ile Cys Gly Leu Arg Gln
545          550          555          560

Leu Ala Asn Glu Thr Thr Gln Ala Leu Gln Leu Phe Leu Arg Ala Thr
          565          570          575

Thr Glu Leu Arg Thr Phe Ser Ile Leu Asn Arg Lys Ala Ile Asp Phe
          580          585          590

Leu Leu Gln Arg Trp Gly Gly Thr Cys His Ile Leu Gly Pro Asp Cys
          595          600          605

Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp Lys Ile Asp
          610          615          620

Gln Ile Ile His Asp Phe Val Asp Lys Thr Leu Pro Asp Gln Gly Asp
625          630          635          640

```

sequence.listing.ST25.txt

Asn Asp Asn Trp Trp Thr Gly Trp Arg Gln Trp Ile Pro Ala Gly Ile
645 650 655

Gly Val Thr Gly Val Ile Ile Ala Val Ile Ala Leu Phe Cys Ile Cys
660 665 670

Lys Phe Val Phe
675

<210> 4
<211> 2030
<212> DNA
<213> Ebola virus glycoprotein

<400> 4
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agcacattac aggttagtga tgtcgacaaa ctggtttgcc gtgacaaact gtcattccacg 180
aatcaattga gatcagttgg actgaatctc gaagggaatg gagtggcaac tgacgtgcca 240
tctgcaacta aaagatgggg cttcaggtcc ggtgtccac caaaagtggc caattatgaa 300
gctggtgaat gggctgaaaa ctgctacaat cttgaaatca aaaaacctga cgggagtgag 360
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caggctaccg gctttggaac caatgagaca gagtatttgt tcgaggttga caatttgacc 720
tacgtccaac ttgaatcaag attcacacca cagtttctgc tccagctgaa tgagacaaga 780
tatacaagtg ggaaaaggag caataccacg ggaaaactaa tttggaaggt caaccccgaa 840
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cagtgtcgca tctgacaacc cttgccacaa tctccacgag tcttcgacct ccataacca 1140
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caactcaagt tgaacaacat caccgcagaa cagacaacgc cagcacaacc tccgacactc 1260
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sequence.listing.ST25.txt

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taattaccaa tactattgct ggagtcgcag gactgatcac aggcgggaga agaactcgaa 1500
gagaagcaat tgtcaatgct caacccaaat gcaaccctaa ttacattac tggactactc 1560
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gccacatttt gggaccggac tgctgtatcg aaccacatga ttggactaag aacataacgg 1860
acaaaattga tcagattatt catgattttg ttgataaaac cttccggac cagggggaca 1920
atgacaattg gtggacagga tggagacagt ggataccggc aggtattgga gttacaggcg 1980
ttataattgc agttatcgct ttattctgta tatgcaaatt tgtcttttag 2030

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<210> 5
<211> 1254
<212> PRT
<213> Ross River Structural polyprotein

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<400> 5

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Met Asn Tyr Ile Pro Thr Gln Thr Phe Tyr Gly Arg Arg Trp Arg Pro
1           5           10           15

```

```

Arg Pro Ala Phe Arg Pro Trp Gln Val Ser Met Gln Pro Thr Pro Thr
          20           25           30

```

```

Met Val Thr Pro Met Leu Gln Ala Pro Asp Leu Gln Ala Gln Gln Met
          35           40           45

```

```

Gln Gln Leu Ile Ser Ala Val Ser Ala Leu Thr Thr Lys Gln Asn Val
          50           55           60

```

```

Lys Ala Pro Lys Gly Gln Arg Gln Lys Lys Gln Gln Lys Pro Lys Glu
65           70           75           80

```

```

Lys Lys Glu Asn Gln Lys Lys Lys Pro Thr Gln Lys Lys Lys Gln Gln
          85           90           95

```

```

Gln Lys Pro Lys Pro Gln Ala Lys Lys Lys Lys Pro Gly Arg Arg Glu
          100          105          110

```

```

Arg Met Cys Met Lys Ile Glu Asn Asp Cys Ile Phe Glu Val Lys Leu
          115          120          125

```

sequence.listing.ST25.txt

Asp Gly Lys Val Thr Gly Tyr Ala Cys Leu Val Gly Asp Lys Val Met
 130 135 140
 Lys Pro Ala His Val Lys Gly Thr Ile Asp Asn Pro Asp Leu Ala Lys
 145 150 155 160
 Leu Thr Tyr Lys Lys Ser Ser Lys Tyr Asp Leu Glu Cys Ala Gln Ile
 165 170 175
 Pro Val His Met Lys Ser Asp Ala Ser Lys Tyr Thr His Glu Lys Pro
 180 185 190
 Glu Gly His Tyr Asn Trp His His Gly Ala Val Gln Tyr Ser Gly Gly
 195 200 205
 Arg Phe Thr Ile Pro Thr Gly Ala Gly Lys Pro Gly Asp Ser Gly Arg
 210 215 220
 Pro Ile Phe Asp Asn Lys Gly Arg Val Val Ala Ile Val Leu Gly Gly
 225 230 235 240
 Ala Asn Glu Gly Ala Arg Thr Ala Leu Ser Val Val Thr Trp Thr Lys
 245 250 255
 Asp Met Val Thr Arg Val Thr Pro Glu Gly Thr Glu Glu Trp Ser Ala
 260 265 270
 Ala Leu Met Met Cys Ile Leu Ala Asn Thr Ser Phe Pro Cys Ser Ser
 275 280 285
 Pro Pro Cys Tyr Pro Cys Cys Tyr Glu Lys Gln Pro Glu Gln Thr Leu
 290 295 300
 Arg Met Leu Glu Asp Asn Val Asn Arg Pro Gly Tyr Tyr Glu Leu Leu
 305 310 315 320
 Glu Ala Ser Met Thr Cys Arg Asn Arg Ser Arg His Arg Arg Ser Val
 325 330 335
 Thr Glu His Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr Leu Ala Tyr
 340 345 350
 Cys Ala Asp Cys Gly Asp Gly Tyr Phe Cys Tyr Ser Pro Val Ala Ile
 355 360 365
 Glu Lys Ile Arg Asp Glu Ala Pro Asp Gly Met Leu Lys Ile Gln Val
 370 375 380

sequence.listing.ST25.txt

Ser Ala Gln Ile Gly Leu Asp Lys Ala Gly Thr His Ala His Thr Lys
385 390 395 400

Ile Arg Tyr Met Ala Gly His Asp Val Gln Glu Ser Lys Arg Asp Ser
405 410 415

Leu Arg Val Tyr Thr Ser Ala Ala Cys Ser Ile His Gly Thr Met Gly
420 425 430

His Phe Ile Val Ala His Cys Pro Pro Gly Asp Tyr Leu Lys Val Ser
435 440 445

Phe Glu Asp Ala Asp Ser His Val Lys Ala Cys Lys Val Gln Tyr Lys
450 455 460

His Asp Pro Leu Pro Val Gly Arg Glu Lys Phe Val Val Arg Pro His
465 470 475 480

Phe Gly Val Glu Leu Pro Cys Thr Ser Tyr Gln Leu Thr Thr Ala Pro
485 490 495

Thr Asp Glu Glu Ile Asp Met His Thr Pro Pro Asp Ile Pro Asp Arg
500 505 510

Thr Leu Leu Ser Gln Thr Ala Gly Asn Val Lys Ile Thr Ala Gly Gly
515 520 525

Arg Thr Ile Arg Tyr Asn Cys Thr Cys Gly Arg Asp Asn Val Gly Thr
530 535 540

Thr Ser Thr Asp Lys Thr Ile Asn Thr Cys Lys Ile Asp Gln Cys His
545 550 555 560

Ala Ala Val Thr Ser His Asp Lys Trp Gln Phe Thr Ser Pro Phe Val
565 570 575

Pro Arg Ala Asp Gln Thr Ala Arg Arg Gly Lys Val His Val Pro Phe
580 585 590

Pro Leu Thr Asn Val Thr Cys Arg Val Pro Leu Ala Arg Ala Pro Asp
595 600 605

Val Thr Tyr Gly Lys Lys Glu Val Thr Leu Arg Leu His Pro Asp His
610 615 620

Pro Thr Leu Phe Ser Tyr Arg Ser Leu Gly Ala Glu Pro His Pro Tyr
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```

625                               630                               635                               640
Glu Glu Trp Val Asp Lys Phe Ser Glu Arg Ile Ile Pro Val Thr Glu
645                               650                               655
Glu Gly Ile Glu Tyr Gln Trp Gly Asn Asn Pro Pro Val Arg Leu Trp
660                               665                               670
Ala Gln Leu Thr Thr Glu Gly Lys Pro His Gly Trp Pro His Glu Ile
675                               680                               685
Ile Gln Tyr Tyr Tyr Gly Leu Tyr Pro Ala Ala Thr Ile Ala Ala Val
690                               695                               700
Ser Gly Ala Ser Leu Met Ala Leu Leu Thr Leu Ala Ala Thr Cys Cys
705                               710                               715                               720
Met Leu Ala Thr Ala Arg Arg Lys Cys Leu Thr Pro Tyr Ala Leu Thr
725                               730                               735
Pro Gly Ala Val Val Pro Leu Thr Leu Gly Leu Leu Cys Cys Ala Pro
740                               745                               750
Arg Ala Asn Ala Ala Ser Phe Ala Glu Thr Met Ala Tyr Leu Trp Asp
755                               760                               765
Glu Asn Lys Thr Leu Phe Trp Met Glu Phe Ala Ala Pro Ala Ala Ala
770                               775                               780
Leu Ala Leu Leu Ala Cys Cys Ile Lys Ser Leu Ile Cys Cys Cys Lys
785                               790                               795                               800
Pro Phe Ser Phe Leu Val Leu Leu Ser Leu Gly Ala Ser Ala Lys Ala
805                               810                               815
Tyr Glu His Thr Ala Thr Ile Pro Asn Val Val Gly Phe Pro Tyr Lys
820                               825                               830
Ala His Ile Glu Arg Asn Gly Phe Ser Pro Met Thr Leu Gln Leu Glu
835                               840                               845
Val Val Glu Thr Ser Trp Glu Pro Thr Leu Asn Leu Glu Tyr Ile Thr
850                               855                               860
Cys Glu Tyr Lys Thr Val Val Pro Ser Pro Phe Ile Lys Cys Cys Gly
865                               870                               875                               880

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sequence.listing.ST25.txt

Thr Ser Glu Cys Ser Ser Lys Glu Gln Pro Asp Tyr Gln Cys Lys Val
885 890 895

Tyr Thr Gly Val Tyr Pro Phe Met Trp Gly Gly Ala Tyr Cys Phe Cys
900 905 910

Asp Ser Glu Asn Thr Gln Leu Ser Glu Ala Tyr Val Asp Arg Ser Asp
915 920 925

Val Cys Lys His Asp His Ala Ser Ala Tyr Lys Ala His Thr Ala Ser
930 935 940

Leu Lys Ala Thr Ile Arg Ile Ser Tyr Gly Thr Ile Asn Gln Thr Thr
945 950 955 960

Glu Ala Phe Val Asn Gly Glu His Ala Val Asn Val Gly Gly Ser Lys
965 970 975

Phe Ile Phe Gly Pro Ile Ser Thr Ala Trp Ser Pro Phe Asp Asn Lys
980 985 990

Ile Val Val Tyr Lys Asp Asp Val Tyr Asn Gln Asp Phe Pro Pro Tyr
995 1000 1005

Gly Ser Gly Gln Pro Gly Arg Phe Gly Asp Ile Gln Ser Arg Thr
1010 1015 1020

Val Glu Ser Lys Asp Leu Tyr Ala Asn Thr Ala Leu Lys Leu Ser
1025 1030 1035

Arg Pro Ser Pro Gly Val Val His Val Pro Tyr Thr Pro Thr Pro
1040 1045 1050

Ser Gly Phe Lys Tyr Trp Leu Lys Glu Lys Gly Ser Ser Leu Asn
1055 1060 1065

Thr Lys Ala Pro Phe Gly Cys Lys Ile Lys Thr Asn Pro Val Arg
1070 1075 1080

Ala Met Asp Cys Ala Val Gly Ser Ile Pro Val Ser Met Asp Ile
1085 1090 1095

Pro Asp Ser Ala Phe Thr Arg Val Val Asp Ala Pro Ala Val Thr
1100 1105 1110

Asp Leu Ser Cys Gln Val Val Val Cys Thr His Ser Ser Asp Phe
1115 1120 1125

sequence.listing.ST25.txt

Gly Gly Val Ala Thr Leu Ser Tyr Lys Thr Asp Lys Pro Gly Lys
1130 1135 1140

Cys Ala Val His Ser His Ser Asn Val Ala Thr Leu Gln Glu Ala
1145 1150 1155

Thr Val Asp Val Lys Glu Asp Gly Lys Val Thr Val His Phe Ser
1160 1165 1170

Thr Ala Ser Ala Ser Pro Ala Phe Lys Val Ser Val Cys Asp Ala
1175 1180 1185

Lys Thr Thr Cys Thr Ala Ala Cys Glu Pro Pro Lys Asp His Ile
1190 1195 1200

Val Pro Tyr Gly Ala Ser His Asn Asn Gln Val Phe Pro Asp Met
1205 1210 1215

Ser Gly Thr Ala Met Thr Trp Val Gln Arg Leu Ala Ser Gly Leu
1220 1225 1230

Gly Gly Leu Ala Leu Ile Ala Val Val Val Leu Val Leu Val Thr
1235 1240 1245

Cys Ile Thr Met Arg Arg
1250

<210> 6
<211> 437
<212> PRT
<213> Ross River Virus E1

<400> 6

Glu His Thr Ala Thr Ile Pro Asn Val Val Gly Phe Pro Tyr Lys Ala
1 5 10 15

His Ile Glu Arg Asn Gly Phe Ser Pro Met Thr Leu Gln Leu Glu Val
20 25 30

Val Glu Thr Ser Leu Glu Pro Thr Leu Asn Leu Glu Tyr Ile Thr Cys
35 40 45

Glu Tyr Lys Thr Val Val Pro Ser Pro Phe Ile Lys Cys Cys Gly Thr
50 55 60

Ser Glu Cys Ser Ser Lys Glu Gln Pro Asp Tyr Gln Cys Lys Val Tyr
65 70 75 80

sequence.listing.ST25.txt

Thr Gly Val Tyr Pro Phe Met Trp Gly Gly Ala Tyr Cys Phe Cys Asp
85 90

Ser Glu Asn Thr Gln Leu Ser Glu Ala Tyr Val Asp Arg Ser Asp Val
100 105 110

Cys Lys His Asp His Ala Ser Ala Tyr Lys Ala His Thr Ala Ser Leu
115 120 125

Lys Ala Thr Ile Arg Ile Ser Tyr Gly Thr Ile Asn Gln Thr Thr Glu
130 135 140

Ala Phe Val Asn Gly Glu His Ala Val Asn Val Gly Gly Ser Lys Phe
145 150 155 160

Ile Phe Gly Pro Ile Ser Thr Ala Trp Ser Pro Phe Asp Asn Lys Ile
165 170 175

Val Val Tyr Lys Asp Asp Val Tyr Asn Gln Asp Phe Pro Pro Tyr Gly
180 185 190

Ser Gly Gln Pro Gly Arg Phe Gly Asp Ile Gln Ser Arg Thr Val Glu
195 200 205

Ser Lys Asp Leu Tyr Ala Asn Thr Ala Leu Lys Leu Ser Arg Pro Ser
210 215 220

Pro Gly Val Val His Val Pro Tyr Thr Gln Thr Pro Ser Gly Phe Lys
225 230 235 240

Tyr Trp Leu Lys Glu Lys Gly Ser Ser Leu Asn Thr Lys Ala Pro Phe
245 250 255

Gly Cys Lys Ile Lys Thr Asn Pro Val Arg Ala Met Asp Cys Ala Val
260 265 270

Gly Ser Ile Pro Val Ser Met Asp Ile Pro Asp Ser Ala Phe Thr Arg
275 280 285

Val Val Asp Ala Pro Ala Val Thr Asp Leu Ser Cys Gln Val Val Val
290 295 300

Cys Thr His Ser Ser Asp Phe Gly Gly Val Ala Thr Leu Ser Tyr Lys
305 310 315 320

Thr Asp Lys Pro Gly Lys Cys Ala Val His Ser His Ser Asn Val Ala
325 330 335

sequence.listing.ST25.txt

Thr Leu Gln Glu Ala Thr Val Asp Val Lys Glu Asp Gly Lys Val Thr
340 345 350

Val His Phe Ser Thr Ala Ser Ala Ser Pro Ala Phe Lys Val Ser Val
355 360 365

Cys Asp Ala Lys Thr Thr Cys Thr Ala Ala Cys Glu Pro Pro Lys Asp
370 375 380

His Ile Val Pro Tyr Gly Ala Ser His Asn Asn Gln Val Phe Pro Asp
385 390 395 400

Met Ser Gly Thr Ala Met Thr Trp Val Gln Arg Leu Ala Ser Gly Leu
405 410 415

Gly Gly Leu Ala Leu Ile Ala Val Val Val Leu Val Leu Val Thr Cys
420 425 430

Ile Thr Met Arg Arg
435

<210> 7
<211> 1311
<212> DNA
<213> Ross River Virus E1

<400> 7
gagcacacag ccacaattcc gaatgtggtg gggttcccgt ataaggctca cattgaaagg 60
aatggcttct cgcccatgac tctgcagctt gaagtgggtg agacaagctt ggaaccacaca 120
cttaacctgg agtacattac ctgcgaatac aagacgggtg tcccttcgcc attcatcaaa 180
tgttgcgga catcagaatg ctcacccaag gagcagccag actaccaatg caaggtgtac 240
acgggtgtat acccattcat gtgggggtgga gcctactgtt tctgcgactc cgagaacacg 300
cagctcagcg aggcctatgt cgacaggtca gacgtttgca aacatgatca cgcacgggcc 360
tacaaggcac acacggcctc tctaaaagca acaatcagga tcagttatgg caccatcaac 420
cagaccaccg aggccttcgt taatgggtgaa cacgcgggtca acgtgggcgg aagcaagttc 480
atctttggac cgatctcaac agcttgggtca ccgttcgaca ataaaattgt cgtgtataaa 540
gatgatgtct acaaccagga cttcccaccc tacggatcag gccagccggg tagattcgga 600
gacattcaga gcaggacagt ggagagcaaa gacttgtatg ccaacacggc cctaaaactc 660
tcaagaccat caccgggggt tgtgcatgtg ccatacacgc agacaccatc cggatttaaa 720
tattggctga aggagaaagg atcttcattg aatacaaagg ccccttttgg ctgcaagata 780
aagaccaatc cagtcagagc catggattgt gcagttggca gtatacctgt gtcgatggac 840

sequence.listing.ST25.txt

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atacctgaca gtgcattcac acgagtggta gatgccccgg ctgtaacaga cctgagctgc   900
caggtagtgg tctgtacaca ctctccgat ttcggaggag ttgccacatt gtcttacaaa   960
acggacaaac ccggcaagtg cgctgtccac tcacattcca acgtcgcaac gttgcaagag  1020
gcgacggtgg atgtcaagga ggatggcaag gtcacagtgc acttttccac ggcgtccgcc  1080
tccccggcct tcaaagtgtc cgtctgtgac gcaaaaacaa cgtgcacggc ggcgtgcgag  1140
cctccaaaag accacatcgt cccttatggg gcgagccata acaaccaggt ctttccggac  1200
atgtcaggaa ctgcatgac gtgggtgcag aggctggcca gtgggttagg tgggctggct  1260
ctcatcgagg tggttgtgct ggtcttggtg acctgcataa caatgcgtcg g          1311

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<210> 8
 <211> 487
 <212> PRT
 <213> Ross River Virus E3-E2

<400> 8

Met Ser Ala Ala Leu Met Met Cys Ile Leu Ala Asn Thr Ser Phe Pro
 1 5 10 15

Cys Ser Ser Pro Pro Cys Tyr Pro Cys Cys Tyr Glu Lys Gln Pro Glu
 20 25 30

Gln Thr Leu Arg Met Leu Glu Asp Asn Val Asn Arg Pro Gly Tyr Tyr
 35 40 45

Glu Leu Leu Glu Ala Ser Met Thr Cys Arg Asn Arg Ser Arg His Arg
 50 55 60

Arg Ser Val Thr Glu His Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr
 65 70 75 80

Leu Ala Tyr Cys Ala Asp Cys Gly Asp Gly Tyr Phe Cys Tyr Ser Pro
 85 90 95

Val Ala Ile Glu Lys Ile Arg Asp Glu Ala Ser Asp Gly Met Leu Lys
 100 105 110

Ile Gln Val Ser Ala Gln Ile Gly Leu Asp Lys Ala Gly Thr His Ala
 115 120 125

His Thr Lys Ile Arg Tyr Met Ala Gly His Asp Val Gln Glu Ser Lys
 130 135 140

Arg Asp Ser Leu Arg Val Tyr Thr Ser Ala Ala Cys Ser Ile His Gly
 145 150 155 160

sequence.listing.ST25.txt

Thr Met Gly His Phe Ile Val Ala His Cys Pro Pro Gly Asp Tyr Leu
 165 170 175
 Lys Val Ser Phe Glu Asp Ala Asp Ser His Val Lys Ala Cys Lys Val
 180 185 190
 Gln Tyr Lys His Asp Pro Leu Pro Val Gly Arg Glu Lys Phe Val Val
 195 200 205
 Arg Pro His Phe Gly Val Glu Leu Pro Cys Thr Ser Tyr Gln Leu Thr
 210 215 220
 Thr Ala Pro Thr Asp Glu Glu Ile Asp Met His Thr Pro Pro Asp Ile
 225 230 235 240
 Pro Asp Arg Thr Leu Leu Ser Gln Thr Ala Gly Asn Val Lys Ile Thr
 245 250 255
 Ala Gly Gly Arg Thr Ile Arg Tyr Asn Cys Thr Cys Gly Arg Asp Asn
 260 265 270
 Val Gly Thr Thr Ser Thr Asp Lys Thr Ile Asn Thr Cys Lys Ile Asp
 275 280 285
 Gln Cys His Ala Ala Val Thr Ser His Asp Lys Trp Gln Phe Thr Ser
 290 295 300
 Pro Phe Val Pro Arg Ala Asp Gln Thr Ala Arg Arg Gly Lys Val His
 305 310 315 320
 Val Pro Phe Pro Leu Thr Asn Val Thr Cys Arg Val Pro Leu Ala Arg
 325 330 335
 Ala Pro Asp Val Thr Tyr Gly Lys Lys Glu Val Thr Leu Arg Leu His
 340 345 350
 Pro Asp His Pro Thr Leu Phe Ser Tyr Arg Ser Leu Gly Ala Glu Pro
 355 360 365
 His Pro Tyr Glu Glu Trp Val Asp Lys Phe Ser Glu Arg Ile Ile Pro
 370 375 380
 Val Thr Glu Glu Gly Ile Glu Tyr Gln Trp Gly Asn Asn Pro Pro Val
 385 390 395 400
 Arg Leu Trp Ala Gln Leu Thr Thr Glu Gly Lys Pro His Gly Trp Pro

sequence.listing.ST25.txt

405

410

415

His Glu Ile Ile Gln Tyr Tyr Tyr Gly Leu Tyr Pro Ala Ala Thr Ile
420 425 430

Ala Ala Val Ser Gly Ala Ser Leu Met Ala Leu Leu Thr Leu Ala Ala
435 440 445

Thr Cys Cys Met Leu Ala Thr Ala Arg Arg Lys Cys Leu Thr Pro Tyr
450 455 460

Ala Leu Thr Pro Gly Ala Val Val Pro Leu Thr Leu Gly Leu Leu Cys
465 470 475 480

Cys Ala Pro Arg Ala Asn Ala
485

<210> 9
<211> 1461
<212> DNA
<213> Ross River Virus E3-E2

<400> 9
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ccctgctacc cctgctgcta cgaaaaacag ccagaacaga cactgcggat gctggaagac 120
aatgtgaata gaccagggtta ctatgagcta ctggaagcgt ccatgacatg cagaaacaga 180
tcacgccacc gccgtagtgt aacagagcac ttcaatgtgt ataaggctac tagaccgtac 240
ttagcgtatt gcgctgactg tggggacggg tacttctgct atagcccagt tgctatcgag 300
aagatccgag atgaggcgctc tgacggcatg ctcaagatcc aagtctccgc ccaaataagg 360
ctggacaagg caggtaccca cgcccacacg aagatccgat atatggctgg tcatgatgtt 420
caggaatcta agagagattc cttgagggtg tacacgtccg cagcgtgctc tatacatggg 480
acgatgggac acttcatcgt cgcacattgt ccgccaggcg actacctcaa ggtttcgttc 540
gaggacgcag attcacacgt gaaggcatgt aagggtccaat acaagcacga cccattgccg 600
gtgggtagag agaagttcgt ggtagaccc cactttggcg tagagctgcc atgcacctca 660
taccagctga caacagctcc caccgacgag gagatcgaca tgcacacacc gccagatata 720
ccggatcgca ccctgctatc acagacggcg ggcaacgtca aaataacagc aggcggcagg 780
actatcaggt acaattgtac ctgtggccgt gacaacgtag gcactaccag tactgacaag 840
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caatttacct ctccatttgt tcccagggt gatcagacag ctaggagggg caaagtgc 960
gttcattcc ctttgactaa cgtcacctgc cgagtgccgt tggctcgagc gccggatgtc 1020

sequence.listing.ST25.txt

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acctatggta agaaggaggt gaccctgaga ttacaccag atcatccgac gctcttctcc 1080
tataggagtt taggagccga accgcacccg tacgaggagt gggttgacaa gttctctgag 1140
cgcatcatcc cagtgcgga agaagggatt gaggaccagt ggggcaacaa cccgccggtc 1200
cgcctatggg cgcaactgac gaccgagggc aaaccccatg gctggccaca tgaaatcatt 1260
cagtactatt atggactata ccccgccgcc accattgccg cagtatccgg ggcgagtctg 1320
atggccctcc taactctagc ggccacatgc tgcagtctgg ccaccgcgag gagaaagtgc 1380
ctaacaccat acgccttgac gccaggagcg gtggtaccgt tgacactggg gctgctttgc 1440
tgcgcaccga gggcgaacgc a 1461

```

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<210> 10
<211> 16
<212> PRT
<213> Marburg glycoprotein C-terminus mutation

```

<400> 10

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Leu Ile Ala Leu Ser Cys Ile Cys Arg Ile Phe Thr Lys Tyr Ile Gly
1           5           10          15

```

```

<210> 11
<211> 16
<212> PRT
<213> Marburg glycoprotein C-terminus mutation

```

<400> 11

```

Leu Ile Ala Leu Ser Ala Ile Cys Arg Ile Phe Thr Lys Tyr Ile Gly
1           5           10          15

```

```

<210> 12
<211> 16
<212> PRT
<213> Marburg glycoprotein C-terminus mutation

```

<400> 12

```

Leu Ile Ala Leu Ser Cys Ile Ala Arg Ile Phe Thr Lys Tyr Ile Gly
1           5           10          15

```

```

<210> 13
<211> 16
<212> PRT
<213> Marburg glycoprotein C-terminus mutation

```

<400> 13

```

Leu Ile Ala Leu Ser Ser Ile Cys Arg Ile Phe Thr Lys Tyr Ile Gly
1           5           10          15

```

```

<210> 14
<211> 16

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sequence.listing.ST25.txt

<212> PRT

<213> Marburg glycoprotein C-terminus mutation

<400> 14

Leu Ile Ala Leu Ser Cys Ile Ser Arg Ile Phe Thr Lys Tyr Ile Gly
1 5 10 15

<210> 15

<211> 13

<212> PRT

<213> Marburg glycoprotein C-terminus mutation

<400> 15

Leu Ile Ala Leu Ser Cys Ile Cys Arg Ile Phe Thr Lys
1 5 10

<210> 16

<211> 10

<212> PRT

<213> Marburg glycoprotein C-terminus mutation

<400> 16

Leu Ile Ala Leu Ser Cys Ile Cys Arg Lys
1 5 10